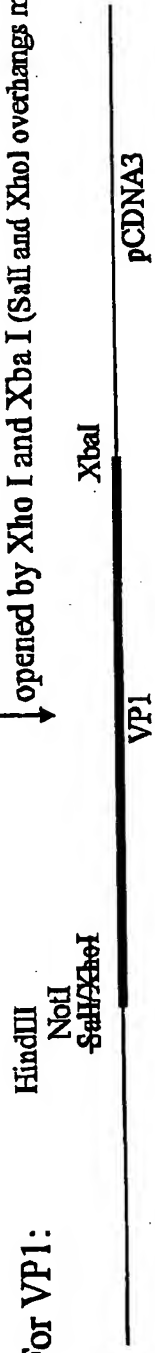
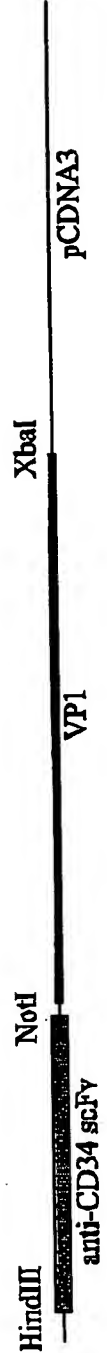


Cloning into pCDNA3
opened by Xho I and Xba I (SalI and XbaI overhangs match!)

For VP1:



Insertion of anti-CD34 scFv into polylinker of pCDNA3
(HindIII and NotI)





2170 2180 2190 2200 2210 2220
TGGATGACTGCATCTTTGAACAATAAATGATTAAATCAGGTATGGCTGCCGATGGTTAT
M A A D G Y 6

XhoI
2230 2240 2250 2260 2270 2280
CTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATAAGACAGTGGTGAAGCTCAAA
L P D W L E D T L S E G I R Q W W K L K₂₆ 26

BsrBI
2290 2300 2310 2320 2330 2340
CCTGGCCCAACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGAGGGGTCTTGTG
P G P P P P K P₃ A E R H K D D S R G L V 46
Vp1 hydro

HindII
2350 2360 2370 2380 2390 2400
CTTCCTGGGTACAAGTACCTCGGACCCTTCAACGGAAGGAGAGCCGGTCAAC
L P G Y K Y L G P F N G L D K G E P V N 66

XhoI
2410 2420 2430 2440 2450 2460
GAGGCAGACGCCGCGGCCCTCGAGCACGACAAAGCCTACGACCGGCAGCTCGACAGCGGA
E A D A A A L E H D K A Y D R Q L D S G 86

2470 2480 2490 2500 2510 2520
GACAACCCGTACCTCAAGTACAACCACGCCGAGGAGTTTCAGGAGCGCCTTAAAGAA
D N P Y L K Y N H A D A E F Q E R L K E 106

2530 2540 2550 2560 2570 2580
GATACGTCTTTTGGGGGCAACCTCGGACGAGCAGTCTTCCAGGCGAAAAAGAGGGTTCTT
D T S F G G N L G R A V F Q A K K R V L 126

START VP2
2590 2600 2610 2620 2630 2640
GAACCTCTGGGCCTGGTTGAGGAACCTGTTAAGACGGCTCCGGGAAAAAAGAGGCCGGTA
E P L G L V E E P V K T A P G K K R P V 146

2650 2660 2670 2680 2690 2700
GAGCACTCTCTGTGGAGCCAGACTCCTCCTCGGGAACCGGAAAGCGGGCCAGCAGCCT
E H S P V E P D S S S G T G K A G Q Q P 166

2710 2720 2730 2740 2750 2760
GCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGACCCCCAG
A R K R L N F G Q T G D A D S V P D P Q 186

START VP3
2770 2780 2790 2800 2810 2820
CCTCTCGGACAGCCACCAAGCAGCGCCCTCTGGTCTGGGAACATAACGATGGCTACAGGC
P L G Q P P A₁₉₃A P₁S₁G₁₂L G T N T M A T G 206
D0

2830 2840 2850 2860 2870 2880
AGTGGCGACCAATGGCAGAGCAATAACGAGGGCGCCGACGGAGTGGGTAATTCCTCGGGA
S G A₂₀₀P₁M₁A₂₁₁D₁N N E G A₂₁₃D₁G₁V₁G₂₂N S S G 226
D1 D2

2890 2900 2910 2920 2930 2940
AATTGGCATTGCGATTCCACATGGATGGGCGACAGAGTCATCAGCACCAGCACC CGAACC
N W H C D S T W M G D R V L₂₄₀F T S T₂₄₄R T 246
D4

2950 2960 2970 2980 2990 3000
TGGGCCCTGCCACCTACAACAACCACCTCTACAAACAAATTTCCAGCCAATCAGGAGCC
W A L P T Y N N H L Y K Q I S S Q S G A 266
ins261

3010 3020 3030 3040 3050 3060
TCGAACGACAATCACTACTTTGGCTACAGCACCCCTTGGGGGTATTTGACTTCAACAGA
S N D N H Y F G Y S T P W G Y F D F N R 286

3070 3080 3090 3100 3110 3120
TTCCACTGCCACTTTTACCACGTGACTGGCAAAGACTCATCAACAACAACTGGGGATTC
F H C H F S P R D W Q R L I N N N W G F 306

3130 3140 3150 3160 3170 3180
CGACCCAAGAGACTCAACTTCAAGCTCTTTAACATTCAAGTCAAAGAGGTACGCAGAAT
R P K R L N F K L F N I Q V K E V T Q N 326

3190 3200 3210 3220 3230 3240
GACGGTACGACGACGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGACTCG
D G T T T I A N N L T S T V Q V F T D S 346

3250 3260 3270 3280 3290 3300
GAGTACCAGCTCCCGTACGTCCTCGGCTCGGCGCATCAAGGATGCCTCCCGCCGTTCCTCA
E Y Q L P Y V L G S A H Q G C L P P F P 366

3310 3320 3330 3340 3350 3360
GCAGACGTCTTCATGGTGCCACAGTATGGATACCTCACCTGAACAACGGGAGTCAGGCA
A D V F M V P Q Y G Y L T L N N G S Q A 386
ins381

3370 3380 3390 3400 3410 3420
GTAGGACGCTCTTCATTTTACTGCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGA
V G R S S F Y C L E Y F P S Q M L R T G 406

3430 3440 3450 3460 3470 3480
AACAACTTTACCTTCAGCTACACTTTTGAGGACGTTCCCTTCCACAGCAGCTACGCTCAC
N N F T F S Y T F E D V P F H S S Y A H 426

3490 3500 3510 3520 3530 3540
AGCCAGAGTCTGGACCGTCTCATGAATCCTCTCATCGACCACTACCTGTATTACTTGAGC
S Q S L D R L M N P L I D Q Y L Y Y L S 446

3550 3560 3570 3580 3590 3600
AGAACAACAACTCCAAGTGAACCAACCAACGAGTCAAGGCTTCAGTTTCTCAGGCCCGGA
R T N T P S G T T T Q S R L Q F S Q A G 466
ins447

3610 3620 3630 3640 3650 3660
GCGAGTGACATTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCCTGTTACCGCCAGCAG

A S D I R D Q S R N W L P G P C Y R Q Q 486

3670 3680 3690 3700 3710 3720
CGAGTATCAAAGACATCTGCGGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACC
R V S K T S A D N N N S E Y S W T G A T 506

3730 3740 3750 3760 3770 3780
AAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCCGCCATGGCAAGCCAC
K Y H L N G R D S L V N P G P A M A S H 526

BsrBI
3790 3800 3810 3820 3830 3840
AAGGACGATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCATCTTTGGAAGCAAGGC
K D D E E K F F P Q S G V L I F G K Q G 546
ins534

3850 3860 3870 3880 3890 3900
TCAGAGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGACGAAGAGGAAATCAGG
S E K T N V D I E K V M I T D E E E I R 566

3910 3920 3930 3940 3950 3960
ACAACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGC
T T N P V A T E Q Y G S V S T N L Q R G 586
ins573

HindII
3970 3980 3990 4000 4010 4020
AACAGACAAGCAGCTACCGCAGATGTCAACACACAAGGCGTTCTTCCAGGCATGGTCTGG
N R Q A A T A D V N T Q G V L P G M V W 606
ins587

4030 4040 4050 4060 4070 4080
CAGGACAGAGATGTGTACCTTCAGGGGCCCATCTGGGCAAAGATTCCACACACGGACGGA
Q D R D V Y L Q G P I W A K I P H T D G 626

4090 4100 4110 4120 4130 4140
CATTTTCACCCCTCTCCCCTCATGGGTGGATTTCGGAATTAACACCCCTCCTCCACAGATT
H F H P S P L M G G F G L K H P P P Q I 646

4150 4160 4170 4180 4190 4200
CTCATCAAGAACACCCCGGTACCTGCGAATCCTTCGACCACCTTCAGTGGCGCAAAGTTT
L I K N T P V P A N P S T T F S A A K F 666

4210 4220 4230 4240 4250 4260
GCTTCCTTCATCACACAGTACTCCACGGGACAGGTTCAGCGTGGAGATCGAGTGGGAGCTG
A S F I T Q Y S T G Q V S V E I E W E L 686

4270 4280 4290 4300 4310 4320
CAGAAGGAAAACAGCAAACGCTGGAATCCCAGAAATTCAGTACACTTCCAACCTACAACAAG
Q K E N S K R W N P E I Q Y T S N Y N K 706

4330 4340 4350 4360 4370 4380
TCTGTTAATGTGGACTTTACTGTGGACACTAATGGCGTGTATTCAGAGCCTCGCCCCATT
S V N V D F T V D T N G V Y S E P R P I 726
ins713

4390 4400 4410 4420 4430 4440
 GGCACCAGATACCTGACTCGTAATCTGTAATTGCTTGTTAATCAATAAACCGTTTAATTC
 G T R Y L T R N L * 735

4450 4460 4470 4480 4490 4500
 GTTTCAGTTGAACTTTGGTCTCTGCGTATTTCTTTCTTATCTAGTTTCCATGGCTACGTA

4510 4520 4530 4540 4550 4560
 GATAAGTAGCATGGCGGGTTAATCATTAACATAACAAGGAACCCCTAGTGATGGAGTTGGCC

4570 4580 4590 4600 4610 4620
 ACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCCGACGC

4630 4640 4650 4660 4670 4680
 CCGGGCTTTGCCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAA

Listed enzymes:

Enzyme Name	No. of cuts	Positions	Recognition sequence
BsrBI	2	2310 3812	gag/cgg
HindII	3	1430 2397 3987	gty/rac
XhoI	2	2233 2419	c/tcgag

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EXHIBIT II